

SEQUENCE LISTING

<110> Chen, Hong
 Silos-Santiago, Immaculada
 <120> NT69, A Novel Nucleoside Transporter
 Family Member And Uses Therefor

<130> MPI2000-433CP1(M)

<150> 09/712797

<151> 2000-11-14

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2625

<212> DNA

<213> Human

<220>

<221> 3'UTR

<222> (1)...(52)

<221> CDS

<222> (53)...(1477)

<221> 5'UTR

<222> (1478)...(2625)

<400> 1

gtcgcacccac gcgtccgctt agaaggagca caggaaagtc ccagaggctg cc atg ggc 58
 Met Gly
 1

tcc gtg ggg agc cag cgc ctt gag gag ccc agc gtg gca ggc aca cca 106
 Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly Thr Pro
 5 10 15

gac ccg ggc gta gtg atg agc ttc ctg ctg cca tac aac agc ttc atc 154
 Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser Phe Ile
 20 25 30

acg gac gtg gac tac ctg cat cac aag tac cca ggg acc tcc atc gtg 202
 Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser Ile Val
 35 40 45 50

ttt gac atg agc ctc acc tac atc ttg gtg gca ctg gca gct gtc ctc 250
 Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Val Leu
 55 60 65

ctg aac aac gtc ctg gtg gag aga ctg acc ctg cac acc agg atc acc 298

Leu	Asn	Asn	Val	Leu	Val	Glu	Arg	Leu	Thr	Leu	His	Thr	Arg	Ile	Thr	
			70					75					80			
gca	ggc	tac	ctc	tta	gcc	ttg	ggc	cct	ctc	ctt	ttt	atc	agc	atc	tgc	346
Ala	Gly	Tyr	Leu	Leu	Ala	Leu	Gly	Pro	Leu	Leu	Phe	Ile	Ser	Ile	Cys	
		85					90					95				
gac	gtg	tgg	ctg	cag	ctc	ttc	tct	cgg	gac	cag	gcc	tac	gcc	atc	aac	394
Asp	Val	Trp	Leu	Gln	Leu	Phe	Ser	Arg	Asp	Gln	Ala	Tyr	Ala	Ile	Asn	
	100					105					110					
ctg	gcc	gct	gtg	ggc	acc	gtg	gcc	ttc	ggc	tgc	aca	gtg	cag	caa	tcc	442
Leu	Ala	Ala	Val	Gly	Thr	Val	Ala	Phe	Gly	Cys	Thr	Val	Gln	Gln	Ser	
115				120						125					130	
agc	ttc	tac	ggg	tac	acg	ggg	atg	ctg	ccc	aag	cgg	tac	acg	cag	ggg	490
Ser	Phe	Tyr	Gly	Tyr	Thr	Gly	Met	Leu	Pro	Lys	Arg	Tyr	Thr	Gln	Gly	
			135					140						145		
gtg	atg	acc	ggg	gag	agc	acg	gcg	ggc	gtg	atg	atc	tct	ctg	agc	cgc	538
Val	Met	Thr	Gly	Glu	Ser	Thr	Ala	Gly	Val	Met	Ile	Ser	Leu	Ser	Arg	
			150					155					160			
atc	ctc	acg	aag	ctg	ctg	ctg	ccc	gac	gag	cgc	gcc	agc	acg	ctc	atc	586
Ile	Leu	Thr	Lys	Leu	Leu	Leu	Pro	Asp	Glu	Arg	Ala	Ser	Thr	Leu	Ile	
		165					170					175				
ttc	ttc	ctg	gtg	tcg	gtg	gcg	ctg	gag	ctg	ctg	tgt	ttc	ctg	ctg	cac	634
Phe	Phe	Leu	Val	Ser	Val	Ala	Leu	Glu	Leu	Leu	Cys	Phe	Leu	Leu	His	
	180					185					190					
ctg	tta	gtg	cgg	cgc	agc	cgc	ttc	gtg	ctc	ttc	tat	acc	aca	cgg	ccg	682
Leu	Leu	Val	Arg	Arg	Ser	Arg	Phe	Val	Leu	Phe	Tyr	Thr	Thr	Arg	Pro	
195				200						205					210	
cgt	gac	agc	cac	cgg	ggc	agg	cca	ggc	ctg	ggc	agg	ggc	tat	ggc	tac	730
Arg	Asp	Ser	His	Arg	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	Tyr	Gly	Tyr	
			215					220						225		
cgc	gtg	cac	cac	gac	gtt	gtc	gcc	ggg	gac	gtc	cac	ttc	gag	cac	cca	778
Arg	Val	His	His	Asp	Val	Val	Ala	Gly	Asp	Val	His	Phe	Glu	His	Pro	
			230					235					240			
gcc	ccg	gcc	ctg	gcc	ccc	aac	gag	tcc	cca	aag	gac	agc	cca	gcc	cac	826
Ala	Pro	Ala	Leu	Ala	Pro	Asn	Glu	Ser	Pro	Lys	Asp	Ser	Pro	Ala	His	
		245				250						255				
gag	gtg	acc	ggc	agc	ggc	ggg	gcc	tac	atg	cgc	ttt	gac	gtg	ccg	cgg	874
Glu	Val	Thr	Gly	Ser	Gly	Gly	Ala	Tyr	Met	Arg	Phe	Asp	Val	Pro	Arg	
	260				265						270					
cca	agg	gtc	cag													

1000 900 800 700 600 500 400 300 200 100 0

	295		300		305	
gtg acc tac ttc atc acg ctg tgc ctg ttc ccc ggc ctc gag tct gag						1018
Val Thr Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu Ser Glu						
	310		315		320	
atc cgc cac tgc atc ctg ggc gag tgg ctg ccc atc ctc atc atg gct						1066
Ile Arg His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile Met Ala						
	325		330		335	
gtg ttc aac ctg tca gac ttc gtg ggc aag atc ctg gca gcc ctg ccc						1114
Val Phe Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala Leu Pro						
	340		345		350	
gtg gac tgg cgg ggc acc cac ctg ctg gcc tgc tcc tgc ctg cgt gtg						1162
Val Asp Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu Arg Val						
	355		360		365	370
gtc ttc atc ccc ctc ttc atc ctg tgc gtc tac ccc agc ggc atg ccc						1210
Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly Met Pro						
	375		380		385	
gcc ctc cgt cac ccc gcc tgg ccc tgc atc ttc tca ctg ctc atg ggc						1258
Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu Met Gly						
	390		395		400	
atc agc aac ggc tac ttc ggc agc gtg ccc atg atc ctg gcg gca ggc						1306
Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala Ala Gly						
	405		410		415	
aaa gtg agc ccc aag cag cgg gag ctg gca ggg aac acc atg acc gtg						1354
Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met Thr Val						
	420		425		430	
tcc tac atg tca ggg ctg acg ctg ggg tcc gcc gtg gcc tac tgc acc						1402
Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr Cys Thr						
	435		440		445	450
tac agc ctc acc cgc gac gct cac ggc agc tgc ctg cac gcc tcc acc						1450
Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala Ser Thr						
	455		460		465	
gcc aat ggt tcc atc ctc gca ggc ctc tgagccagcc ccgcccactg						1497
Ala Asn Gly Ser Ile Leu Ala Gly Leu						
	470		475			
ccagggacgc cgagggcctg accagggggcc ccgaggcctg agggcccctc ccctgtcccc						1557
acctcagtgc ctgcgggggcc ctgagcctcc ccctgtgccg gcagccccac tccctcaggg						1617
tccagccatg ccccaccctg gactgaagtt ctgcaaagtc ctccgaggac cggaacacgt						1677
ttctgcgacc cggggctctg gccagcactg tggtctgctg ttggtctcat acctgcgtct						1737
accttccatc tgtgtccagc ggccccggct ccagcccagc cagcactctg cagggtcaca						1797
cgcaccgtgt ccccacccag gacagcagac acccgccaga gtgtgcgcgc ccagtgcactg						1857
caccccggcc ctcatcacc accggcactg atcggggcac cgctggccc agcctccacc						1917
agggaccctt cctcatgaac tctggagccc tgagaggaga ggggcagccc cccacctgtg						1977
caccctcagg gcttcccctt ctgtcctcat tcttagagac tgcttctccc aaacataacg						2037
cgttagccat gaaggagtcg gagccctggg tccgaatgga cccgcctgcg gtctgcatca						2097
gcctctggga aaccacagca gtgatgccag ctgggcacgt caggacctcc ccacacaccc						2157

```

acacgatgcc acaggtcagg gggctgtgcc tgactaggga gccctcccat tgccttcctg 2217
gcccgggata gaagagggga ggtaagtctg ggggctacga agccggggccc ccacaccctg 2277
gctgaagtca gcttgaccta ggtcttgacc ctcattccagc aagggactcg acagacccaa 2337
gggtccctgg aacgtaggga ggggctgggg gtcactccag cccggggcctc ccagaacacc 2397
aggcccggtg ggggtggcacc ctgaggtcag gggatcctaa ggggtgcctt ccagagacgg 2457
tgtttccagg gggaggaccg cccccgcttc cagatccccg gccccggctg tgactgcctt 2517
gtttcacccc tgctgtgtcc catccccgt ctgtccacta actgtaccgc accggccatt 2577
aaaagatgaa ggcagaccgc tgcaaaaaaa aaaaaaaagg gcggccgc 2625

```

<210> 2

<211> 475

<212> PRT

<213> Human

<400> 2

```

Met Gly Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly
1          5          10          15
Thr Pro Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser
20          25          30
Phe Ile Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser
35          40          45
Ile Val Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala
50          55          60
Val Leu Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg
65          70          75          80
Ile Thr Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser
85          90          95
Ile Cys Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala
100         105         110
Ile Asn Leu Ala Ala Val Gly Thr Val Ala Phe Gly Cys Thr Val Gln
115         120         125
Gln Ser Ser Phe Tyr Gly Tyr Thr Gly Met Leu Pro Lys Arg Tyr Thr
130         135         140
Gln Gly Val Met Thr Gly Glu Ser Thr Ala Gly Val Met Ile Ser Leu
145         150         155         160
Ser Arg Ile Leu Thr Lys Leu Leu Leu Pro Asp Glu Arg Ala Ser Thr
165         170         175
Leu Ile Phe Phe Leu Val Ser Val Ala Leu Glu Leu Leu Cys Phe Leu
180         185         190
Leu His Leu Leu Val Arg Arg Ser Arg Phe Val Leu Phe Tyr Thr Thr
195         200         205
Arg Pro Arg Asp Ser His Arg Gly Arg Pro Gly Leu Gly Arg Gly Tyr
210         215         220
Gly Tyr Arg Val His His Asp Val Val Ala Gly Asp Val His Phe Glu
225         230         235         240
His Pro Ala Pro Ala Leu Ala Pro Asn Glu Ser Pro Lys Asp Ser Pro
245         250         255
Ala His Glu Val Thr Gly Ser Gly Gly Ala Tyr Met Arg Phe Asp Val
260         265         270
Pro Arg Pro Arg Val Gln Arg Ser Trp Pro Thr Phe Arg Ala Leu Leu
275         280         285
Leu His Arg Tyr Val Val Ala Arg Val Ile Trp Ala Asp Met Leu Ser
290         295         300
Ile Ala Val Thr Tyr Phe Ile Thr Leu Cys Leu Phe Pro Gly Leu Glu
305         310         315         320
Ser Glu Ile Arg His Cys Ile Leu Gly Glu Trp Leu Pro Ile Leu Ile
325         330         335

```

Met Ala Val Phe Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala
340 345 350
Leu Pro Val Asp Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu
355 360 365
Arg Val Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly
370 375 380
Met Pro Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu
385 390 395 400
Met Gly Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala
405 410 415
Ala Gly Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met
420 425 430
Thr Val Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr
435 440 445
Cys Thr Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala
450 455 460
Ser Thr Ala Asn Gly Ser Ile Leu Ala Gly Leu
465 470 475

<210> 3
<211> 1428
<212> DNA
<213> Human

<220>
<221> CDS
<222> (1)...(1428)

<400> 3
atg ggc tcc gtg ggg agc cag cgc ctt gag gag ccc agc gtg gca ggc 48
Met Gly Ser Val Gly Ser Gln Arg Leu Glu Glu Pro Ser Val Ala Gly
1 5 10 15
aca cca gac ccg ggc gta gtg atg agc ttc ctg ctg cca tac aac agc 96
Thr Pro Asp Pro Gly Val Val Met Ser Phe Leu Leu Pro Tyr Asn Ser
20 25 30
ttc atc acg gac gtg gac tac ctg cat cac aag tac cca ggg acc tcc 144
Phe Ile Thr Asp Val Asp Tyr Leu His His Lys Tyr Pro Gly Thr Ser
35 40 45
atc gtg ttt gac atg agc ctc acc tac atc ttg gtg gca ctg gca gct 192
Ile Val Phe Asp Met Ser Leu Thr Tyr Ile Leu Val Ala Leu Ala Ala
50 55 60
gtc ctc ctg aac aac gtc ctg gtg gag aga ctg acc ctg cac acc agg 240
Val Leu Leu Asn Asn Val Leu Val Glu Arg Leu Thr Leu His Thr Arg
65 70 75 80
atc acc gca ggc tac ctc tta gcc ttg ggc cct ctc ctt ttt atc agc 288
Ile Thr Ala Gly Tyr Leu Leu Ala Leu Gly Pro Leu Leu Phe Ile Ser
85 90 95
atc tgc gac gtg tgg ctg cag ctc ttc tct cgg gac cag gcc tac gcc 336
Ile Cys Asp Val Trp Leu Gln Leu Phe Ser Arg Asp Gln Ala Tyr Ala
100 105 110

bioRxiv preprint doi: <https://doi.org/10.1101/1428>; this version posted May 1, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

atc Ile	aac Asn	ctg Leu	gcc Ala	gct Ala	gtg Val	ggc Gly	acc Thr	gtg Val	gcc Ala	ttc Phe	ggc Gly	tgc Cys	aca Thr	gtg Val	cag Gln	384
115120125																
caa Gln	tcc Ser	agc Ser	ttc Phe	tac Tyr	ggg Gly	tac Tyr	acg Thr	ggg Gly	atg Met	ctg Leu	ccc Pro	aag Lys	cgg Arg	tac Tyr	acg Thr	432
130135140																
cag Gln	ggg Gly	gtg Val	atg Met	acc Thr	ggg Gly	gag Glu	agc Ser	acg Thr	gcg Ala	ggc Gly	gtg Val	atg Met	atc Ile	tct Ser	ctg Leu	480
145150155160																
agc Ser	cgc Arg	atc Ile	ctc Leu	acg Thr	aag Lys	ctg Leu	ctg Leu	ctg Leu	ccc Pro	gac Asp	gag Glu	cgc Arg	gcc Ala	agc Ser	acg Thr	528
165170175																
ctc Leu	atc Ile	ttc Phe	ttc Phe	ctg Leu	gtg Val	tgc Ser	gtg Val	gcg Ala	ctg Leu	gag Glu	ctg Leu	ctg Leu	tgt Cys	ttc Phe	ctg Leu	576
180185190																
ctg Leu	cac His	ctg Leu	tta Leu	gtg Val	cgg Arg	cgc Arg	agc Ser	cgc Arg	ttc Phe	gtg Val	ctc Leu	ttc Phe	tat Tyr	acc Thr	aca Thr	624
195200205																
cgg Arg	ccg Pro	cgt Arg	gac Asp	agc Ser	cac His	cgg Arg	ggc Gly	agg Arg	cca Pro	ggc Gly	ctg Leu	ggc Gly	agg Arg	ggc Gly	tat Tyr	672
210215220																
ggc Gly	tac Tyr	cgc Arg	gtg Val	cac His	cac His	gac Asp	gtt Val	gtc Val	gcc Ala	ggg Gly	gac Asp	gtc Val	cac His	ttc Phe	gag Glu	720
225230235240																
cac His	cca Pro	gcc Ala	ccg Pro	gcc Ala	ctg Leu	gcc Ala	ccc Pro	aac Asn	gag Glu	tcc Ser	cca Pro	aag Lys	gac Asp	agc Ser	cca Pro	768
245250255																
gcc Ala	cac His	gag Glu	gtg Val	acc Thr	ggc Gly	agc Ser	ggc Gly	ggg Gly	gcc Ala	tac Tyr	atg Met	cgc Arg	ttt Phe	gac Asp	gtg Val	816
260265270																
ccg Pro	cgg Arg	cca Pro	agg Arg	gtc Val	cag Gln	cgc Arg	agc Ser	tgg Trp	ccc Pro	acc Thr	ttc Phe	aga Arg	gcc Ala	ctg Leu	tta Leu	864
275280285																
ctg Leu	cac His	cgc Arg	tac Tyr	gtg Val	gtg Val	gcg Ala	cgg Arg	gtg Val	atc Ile	tgg Trp	gcc Ala	gac Asp	atg Met	ctc Leu	tcc Ser	912
290295300																
atc Ile	gcc Ala	gtg Val	acc Thr	tac Tyr	ttc Phe	atc Ile	acg Thr	ctg Leu	tgc Cys	ctg Leu	ttc Phe	ccc Pro	ggc Gly	ctc Leu	gag Glu	960
305310315320																
tct Ser	gag Glu	atc Ile	cgc Arg	cac His	tgc Cys	atc Ile	ctg Leu	ggc Gly	gag Glu	tgg Trp	ctg Leu	ccc Pro	atc Ile	ctc Leu	atc Ile	1008
325330335																

atg gct gtg ttc aac ctg tca gac ttc gtg ggc aag atc ctg gca gcc	1056
Met Ala Val Phe Asn Leu Ser Asp Phe Val Gly Lys Ile Leu Ala Ala	
340 345 350	
ctg ccc gtg gac tgg cgg ggc acc cac ctg ctg gcc tgc tcc tgc ctg	1104
Leu Pro Val Asp Trp Arg Gly Thr His Leu Leu Ala Cys Ser Cys Leu	
355 360 365	
cgt gtg gtc ttc atc ccc ctc ttc atc ctg tgc gtc tac ccc agc ggc	1152
Arg Val Val Phe Ile Pro Leu Phe Ile Leu Cys Val Tyr Pro Ser Gly	
370 375 380	
atg ccc gcc ctc cgt cac ccc gcc tgg ccc tgc atc ttc tca ctg ctc	1200
Met Pro Ala Leu Arg His Pro Ala Trp Pro Cys Ile Phe Ser Leu Leu	
385 390 395 400	
atg ggc atc agc aac ggc tac ttc ggc agc gtg ccc atg atc ctg gcg	1248
Met Gly Ile Ser Asn Gly Tyr Phe Gly Ser Val Pro Met Ile Leu Ala	
405 410 415	
gca ggc aaa gtg agc ccc aag cag cgg gag ctg gca ggg aac acc atg	1296
Ala Gly Lys Val Ser Pro Lys Gln Arg Glu Leu Ala Gly Asn Thr Met	
420 425 430	
acc gtg tcc tac atg tca ggg ctg acg ctg ggg tcc gcc gtg gcc tac	1344
Thr Val Ser Tyr Met Ser Gly Leu Thr Leu Gly Ser Ala Val Ala Tyr	
435 440 445	
tgc acc tac agc ctc acc cgc gac gct cac ggc agc tgc ctg cac gcc	1392
Cys Thr Tyr Ser Leu Thr Arg Asp Ala His Gly Ser Cys Leu His Ala	
450 455 460	
tcc acc gcc aat ggt tcc atc ctc gca ggc ctc tga	1428
Ser Thr Ala Asn Gly Ser Ile Leu Ala Gly Leu *	
465 470 475	

1000 2000 3000 4000 5000 6000 7000 8000 9000 10000 11000 12000 13000 14000 15000 16000 17000 18000 19000 20000 21000 22000 23000 24000 25000 26000 27000 28000 29000 30000 31000 32000 33000 34000 35000 36000 37000 38000 39000 40000 41000 42000 43000 44000 45000 46000 47000 48000 49000 50000 51000 52000 53000 54000 55000 56000 57000 58000 59000 60000 61000 62000 63000 64000 65000 66000 67000 68000 69000 70000 71000 72000 73000 74000 75000 76000 77000 78000 79000 80000 81000 82000 83000 84000 85000 86000 87000 88000 89000 90000 91000 92000 93000 94000 95000 96000 97000 98000 99000 100000